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Bacteriological profile of chronic osteomyelitis in a tertiary care hospital in South India

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Background: Chronic osteomyelitis (COM) is a major medical problem in most countries, mainly associated with violent trauma, modern surgery and inadequate treatment of acute osteomyelitis. Although the incidence of osteomyelitis has reduced to a certain extent with the advent of antibiotics and chemotherapeutic agents, yet it continues to be a major problem in India.

Methods & Materials: A retrospective analysis of data of purulent (Pus/pus swabs, tissue) specimen received from patients with chronic osteomyelitis by the microbiology department between January 2013-0ctober 2015 was carried out. The samples were processed using standard microbiological techniques. Identification and antimicrobial susceptibility pattern of the bacterial isolates were done using the Vitek 2 (*bioMerieux, Marcy l'Etoile- France*) system.

Results: In all, 184 patients with chronic osteomyelitis were documented during the study period. There was a male preponderance (163 / 184, 88.5%) with majority, in the age group of 10-20 years. Trauma was the major risk factor for osteomyelitis (95/ 184, 51.6%). The lower limb bones were more commonly affected of which femur (166/184, 90.2%) was the predominant bone involved. Culture was positive in 104/184 (56.6%), with the Gram positive organisms most predominant. MRSA was the predominant organism isolated in 28/104 (27%) cases. Among Gram negative bacilli, *Escherichia coli* was most common organism isolated in 11/104 (10.4%). Other organisms isolated included *Pseudomonas aeruginosa, Klebsiella pneumonia, Acinetobacter baumanii, Proteus mirabilis, Enterobacter cloacae, Morganella morgagnii* and showed a high level of antibiotic resistance. In this study no anaerobic organisms were isolated. One patient had a mixed infection with *Mycobacterium tuberculosis* and *A.baumannii.* Majority of the patients (85/184, 46%) were managed conservatively with wound care and antibiotics. No mortality was recorded.

Conclusion: Prognosis of chronic osteomyelitis depends on proper microbiological techniques that help in isolation, identification and treatment of the bone-infecting, often multidrug resistant organism. Complications can be further reduced with surgical debridement and removal of the dead tissues.

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Characterization of diarrhoegenic escherichia coli using a novel multiplex PCR

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Background: Diarrheal diseases are the second most common cause of infant mortality and morbidity in children less than five years of age. Among all the diarrheal pathogens, Diarrhoegenic *Escherichia coli* (DEC) plays an important role in epidemic and endemic diarrhea. For the identification of these pathogens, serotypic markers may correlate but are rarely reliably sufficient in identifying a strain as diarrheagenic. PCR targeting the virulence factors is a reliable and rapid way of detecting DEC. This study was undertaken to characterize DEC with diarrhea using multiplex PCR DEC and to obtain the clinico- microbiological profile of the infection.

Methods & Materials: One hundred and twenty children below 5 years of age with diarrhea attending Paediatric department were enrolled in our study after obtaining written informed consent of their parents or guardians for a period of two years from October 2013 to October 2015. Fecal samples were collected from these children. Escherichia coli isolates grown were identified by biochemical reactions. A multiplex PCR was developed to detect the virulence genes (*aggR, eaeA, bfpA, ial, lt, st, stx1* and *stx2*) of various pathotypes of DEC.

Results: Among all, 45 samples had DEC. Of them 21(49%) were Enteropatogenic *E.coli*, 6(13.3%) were Enterotoxigenic *E.coli*, 5 (11%) were Enteroaggregative *E.coli*, 4(9%) were Enterohaemorrhagic *E.coli* and 3(6.6%) were Enteroinvasive *E.coli*. We also found in our study 3(6.6%) hybrid strains (2 were atypicalEPEC and EAEC and 1 was EIEC with EHEC) and 3(6.6%) mixed infections {EAEC and EIEC, typical EPEC and EHEC, EAEC and atypical EPEC). Out of 22 EPEC positive samples, 5 (22%) were identified as atypical EPEC as they possessed *eaeA* only and not *bfpA*,3 (13.6%) isolates were identified as typical as they possessed both *eaeA* and *bfpA* genes, while 13 isolates(59%) possessed only *bfpA* gene. The majority (90%) of cases of EPEC diarrhea clustered in the less than two years age group.

Conclusion: This multiplex PCR technology will serve as a good epidemiological tool for the screening of pathotypes of DEC that causes diarrhea in children.

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